

P1009PC00

1

SEQUENCE LISTING

<110> M&E Biotech A/S

<120> Novel Method For Down-Regulation Of Amyloid

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<170> PatentIn Ver. 3.0

<210> 1

<211> 2313

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (2098)..(2169)

<223> nucleotides encoding transmembrane region

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<222> (2014)..(2313)

<223> Nucleotides encoding C-100

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<222> (2016)..(2144)

<223> Abeta 42/43

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gcg	ctg	gag	gta	ccc	act	gat	ggt	aat	gct	ggc	ctg	ctg	gct	gaa	ccc	96
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro	
			20					25					30			

cag	att	gcc	atg	ttc	tgt	ggc	aga	ctg	aac	atg	cac	atg	aat	gtc	cag	144
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln	
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aat	ggg	aag	tgg	gat	tca	gat	cca	tca	ggg	acc	aaa	acc	tgc	att	gat	192
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	
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acc	aag	gaa	ggc	atc	ctg	cag	tat	tgc	caa	gaa	gtc	tac	cct	gaa	ctg	240
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	
	65				70					75				80		

cag	atc	acc	aat	gtg	gta	gaa	gcc	aac	caa	cca	gtg	acc	atc	cag	aac	288
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
			85					90					95			

tgg	tgc	aag	cgg	ggc	cgc	aag	cag	tgc	aag	acc	cat	ccc	cac	ttt	gtg	336
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
			100				105						110			

att	ccc	tac	cgc	tgc	tta	gtt	ggt	gag	ttt	gta	agt	gat	gcc	ctt	ctc	384
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
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gtt	cct	gac	aag	tgc	aaa	ttc	tta	cac	cag	gag	agg	atg	gat	gtt	tgc	432
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
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Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe	
305 310 315 320	
tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac	1008
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr	
325 330 335	
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act	1056
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr	
340 345 350	
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca	1104
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala	
355 360 365	
gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat	1152
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp	
370 375 380	
gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc	1200
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala	
385 390 395 400	
aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca	1248
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala	
405 410 415	
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc	1296
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile	
420 425 430	
cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac	1344
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn	
435 440 445	
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg	1392
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met	
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Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val	
625 630 635 640	
gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct	1968
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser	
645 650 655	
ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat	2016
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp	
660 665 670	
gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg	2064
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu	
675 680 685	
gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga	2112
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly	
690 695 700	
ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg	2160
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu	
705 710 715 720	
gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg	2208
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val	
725 730 735	
gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg	2256
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met	
740 745 750	
cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg	2304
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met	
755 760 765	
cag aac tag	2313
Gln Asn	
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<212> PRT

<213> Homo sapiens

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20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

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Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
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Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
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Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

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10

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
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Gln Asn
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1 5 10 15

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